

## SEQUENCE LISTING

09/674330  
584 BLS GPC/PTC 30 OCT 2000

&lt;110&gt; Ono Pharmaceutical Co., Ltd.

<120> A novel polypeptide, a cDNA encoding the polypeptide  
and utilization thereof

&lt;130&gt; Q61536

&lt;140&gt;

&lt;141&gt;

&lt;150&gt; PCT/JP99/02283

&lt;151&gt; 1999-04-28

&lt;150&gt; JP HEI 10-119731

&lt;151&gt; 1998-04-28

&lt;160&gt; 12

&lt;170&gt; PatentIn Ver. 2.1

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&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;400&gt; 1

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        embryonic heart

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Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser	
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Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln	
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Gln Tyr Pro Phe	
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<213> Mus musculus

<223> Clone mouse A55 derived from Day 13 mouse  
 embryonic heart

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Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr  
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 Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala  
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 Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val  
 75 80 85  
 Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val  
 90 95 100 105  
 Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys  
 110 115 120  
 Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp  
 125 130 135  
 Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr  
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 Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu  
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 Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe  
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 Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp  
 250 255 260 265  
 Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr  
 270 275 280  
 Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys  
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Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala  
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Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp  
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Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met  
330 335 340 345

Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys  
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Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile  
365 370 375

Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile  
380 385 390

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Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser  
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Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro  
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Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu

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90

95

Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln  
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Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys  
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Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile  
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Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro  
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Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp  
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Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys  
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Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp  
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Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp  
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Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln  
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Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp  
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Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys  
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Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu  
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Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala



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345

350

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Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val  
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175 180 185 190	
gag aat ccc tgt gtt cag acc tgt gtc aac acc tat ggc tct ttc atc	957
Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile	
195 200 205	
tgc cgc tgt gac cca gga tat gaa ctt gag gaa gat ggc att cac tgc	1005
Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys	
210 215 220	
agt gat atg gac gag tgc agc ttc tcc gag ttc ctc tgt caa cac gag	1053
Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu	
225 230 235	
tgt gtg aac cag ccg ggc tca tac ttc tgc tgg tgc cct cca ggc tac	1101
Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr	
240 245 250	
gtc ctg ttg gat gat aac cga agc tgc cag gat atc aat gaa tgt gag	1149
Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu	
255 260 265 270	
cac cga aac cac acc tgt acc tca ctg cag act tgc tac aat cta caa	1197
His Arg Asn His Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln	
275 280 285	

ggg ggc ttc aaa tgt att gat ccc atc agc tgt gag gag cct tat ctg 1245  
 Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu  
 290 295 300

ctg att ggt gaa aac cgc tgt atg tgt cct gct gag cac acc agc tgc 1293  
 Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys  
 305 310 315

aga gac cag cca ttc acc atc ctg tat cgg gac atg gat gtg gtg tca 1341  
 Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser  
 320 325 330

gga cgc tcc gtt cct gct gac atc ttc cag atg caa gca aca acc cga 1389  
 Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg  
 335 340 345 350

tac cct ggt gcc tat tac att ttc cag atc aaa tct ggc aac gag ggt 1437  
 Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly  
 355 360 365

cga gag ttc tat atg cgg caa aca ggg cct atc agt gcc acc ctg gtg 1485  
 Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val  
 370 375 380

atg aca cgc ccc atc aaa ggg cct cgg gac atc cag ctg gac ttg gag 1533  
 Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu  
 385 390 395

atg atc act gtc aac act gtc atc aac ttc aga ggc agc tcc gtg atc 1581  
 Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile  
 400 405 410

cga ctg cgg ata tat gtg tgc cag tat ccg ttc tgagcctctg gctaaggcct 1634  
 Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe  
 415 420 425

ctgacactgc ctttcaccag caccgaggga cgggaggaga aaggaaacca gcaagaatga 1694

gagcgagaca gacattgcac ctttctgtgt gaatatctcc tggggggcacc agcctagcat 1754

cttgacccat atctgtacta ttgcagatgg tcaactctgaa ggacaccctg ccctcagttc 1814

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gggggtatgag tcttcgaagg ttcaaaaagac tgagtggctt gctctcacct cttcctctcc 1994

ttctccatc tcttgctgca ttgctgcttt gcaaaagtc tcatgggctc gtgggaaatg 2054  
 ctgggaatag ctagtcttgc tcttgcatgt tctgagaagg ctatgggaac acaccacagc 2114  
 aggatcgaag gtttttatag agtctatttt aaaatcacat ctggtatttt cagcataaaa 2174  
 gaaatttttag ttgtctttaa aatttgtag agtggttaac cttttcttat tcattttgag 2234  
 gctttctaaa gtggtagaat tctttccaaa ggctcagat acatgttatg ttcagtcttt 2294  
 ccaacctcat cctttctgc atcttagccc agtttttacg aagacctctt aatcatgctt 2354  
 tnttaagagt ttttacccaa ctgcgttgga agacagaggt atccagactg attaaataat 2414  
 tgaagaaaaa aaaaaa 2429

<210> 8  
 <211> 461  
 <212> PRT  
 <213> Mus musculus  
 <223> Clone mouse A55b derived from Day 13 mouse  
 embryonic heart

<400> 8  
 Met Gly Pro Arg Ser Phe Glu Pro Met His Ser Gly Leu Cys Arg Gln  
 -35 -30 -25  
 Arg Arg Met Ile Leu Thr Val Thr Ile Leu Ala Leu Trp Leu Pro His  
 -20 -15 -10 -5  
 Pro Gly Asn Ala Gln Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg  
 -1 1 5 10  
 Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu  
 15 20 25  
 Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu  
 30 35 40  
 Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro  
 45 50 55 60  
 Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val  
 65 70 75  
 Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val Cys Arg Phe  
 80 85 90

Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val Asp Glu Cys  
95 100 105

Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr  
110 115 120

Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu  
125 130 135 140

Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln  
145 150 155

Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly  
160 165 170

Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys  
175 180 185

Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser  
190 195 200

Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile  
205 210 215 220

His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln  
225 230 235

His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro  
240 245 250

Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu  
255 260 265

Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn  
270 275 280

Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro  
285 290 295 300

Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala Glu His Thr  
305 310 315

Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val  
320 325 330

Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr  
335 340 345

Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn  
 350 355 360

Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr  
 365 370 375 380

Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp  
 385 390 395

Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser  
 400 405 410

Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe  
 415 420 425

\*210\* 9

\*211\* 423

\*212\* PRT

\*213\* Mus musculus

\*400\* 9

Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu  
 1 5 10 15

Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met  
 20 25 30

Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn  
 35 40 45

Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser  
 50 55 60

Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro  
 65 70 75 80

Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu  
 85 90 95

Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln  
 100 105 110

Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys  
 115 120 125



Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile  
130 135 140

Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro  
145 150 155 160

Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp  
165 170 175

Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys  
180 185 190

Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp  
195 200 205

Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp  
210 215 220

Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln  
225 230 235 240

Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp  
245 250 255

Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His  
260 265 270

Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys  
275 280 285

Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu  
290 295 300

Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro  
305 310 315 320

Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val  
325 330 335

Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala  
340 345 350

Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr  
355 360 365

Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro  
370 375 380

Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val  
 385 390 395 400

Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile  
 405 410 415

Tyr Val Ser Gln Tyr Pro Phe  
 420

<210> 10  
 <211> 1269  
 <212> DNA  
 <213> Mus musculus

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 tgccggacca tccctgaggg ttgtcgtggg gacatgatgt gtgtcaacca gaatggcggg 120  
 tatttgtgca tccctcgaac caacccagtg tatcgagggc cttactcaaa tccctactct 180  
 acatcctact caggcccata cccagcagcg gcccaccag taccagcttc caactacccc 240  
 acgatttcaa ggccctctgt ctgccgcttt gggatcaga tggatgaagg caaccagtggt 300  
 gtggatgtgg acgagtgtgc aacagactca caccagtgc accctaccca gatctgtatc 360  
 aacactgaag gaggttacac ctgctcctgc accgatgggt actggcttct ggaagggcag 420  
 tgccctagata ttgatgaatg tcgctatggg tactgccagc agctctgtgc aaatgttcca 480  
 ggatcctatt cctgtacatg caaccctggg ttcacctca acgacgatgg aaggtcttgc 540  
 caagatgtga acgagtgcga aactgagaat ccctgtgttc agacctgtgt caacacctat 600  
 ggctctttca tctgccgctg tgaccagga tatgaacttg aggaagatgg cattcactgc 660  
 agtgaatatg acgagtgcag cttctccgag ttctctgtc aacacgagtg tgtgaaccag 720  
 ccgggctcat acttctgtc gtgccctcca ggctacgtcc tgttgatga taaccgaagc 780  
 tgccaggata tcaatgaatg tgagaccga aaccacacgt gtacctact gcagacttgc 840  
 tacaatctac aagggggctt caaatgtatt gatcccatca gctgtgagga gccttatctg 900  
 ctgattgggtg aaaaccgctg tatgtgtcct gctgagcaca ccagctgcag agaccagcca 960  
 ttcaccatcc tgtatcggga catggatgtg gtgtcaggac gctccgttcc tgctgacatc 1020  
 ttccagatgc aagcaacaac ccgataccct ggtgcctatt acattttcca gatcaaactc 1080  
 ggcaacgagg gtcgagagtt ctatatgagg caaacagggc ctatcagtgc caccctgggtg 1140  
 atgacacgcc ccatcaaagg gctcggggac atccagctgg acttggagat gatcactgtc 1200  
 aacactgtca tcaacttcag aggcagctcc gtgatccgac tgcggatata tgtgtcgcag 1260  
 taccgcttc 1269

<210> 11  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 11  
cgattgaatt ctagacctgc ctcgagnnnn nnnnn

35

<210> 12  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: mA55 R1 Primer

<400> 12  
cgtttgtagc ctgctgctgt gcattcc

27